OIPE

RAW SEQUENCE LISTING   DATE: 10/21/2002
PATENT APPLICATION: US/09/997,425   TIME: 16:04:02

Input Set : **A:\Cura475c.app**
Output Set: **N:\CRF4\10212002\I997425.raw**

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 3 <110> APPLICANT: Edinger et al.
 5 <120> TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
 7 <130> FILE REFERENCE: 21402-175CIP1
 9 <140> CURRENT APPLICATION NUMBER: 09/997,425
10 <141> CURRENT FILING DATE: 2001-11-29
12 <150> PRIOR APPLICATION NUMBER: 60/242,485
13 <151> PRIOR FILING DATE: 2000-10-23
15 <150> PRIOR APPLICATION NUMBER: 60/263,339
16 <151> PRIOR FILING DATE: 2001-01-22
18 <150> PRIOR APPLICATION NUMBER: 60/264,850
19 <151> PRIOR FILING DATE: 2001-01-29
21 <150> PRIOR APPLICATION NUMBER: 10/035,568
22 <151> PRIOR FILING DATE: 2001-10-22
24 <160> NUMBER OF SEQ ID NOS: 92
26 <170> SOFTWARE: PatentIn Ver. 2.1
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29 <211> LENGTH: 1747
30 <212> TYPE: DNA
31 <213> ORGANISM: Homo sapiens
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36 acactggcag ctggagatgg cggacacgag atccgtgcac gagactaggt ttgaggcggc 180
37 cgtgaaggtg atccagagtt tgccgaagaa tggttcattc cagccaacaa atgaaatgat 240
38 gcttaaattt tatagcttct ataagcaggc aactgaagga ccctgtaaac tttcaaggcc 300
39 tggattttgg gatcctattg gaagatataa atgggatgct tggagttcac tgggtgatat 360
40 gaccaaagag gaagccatga ttgcatatgt tgaagaaatg aaaaagatta ttgaaactat 420
41 gccaatgact gagaaagttg aagaattgct gcgtgtcata ggtccatttt atgaaattgt 480
42 cgaggacaaa aagagtggca ggagttctga tataacctca gatcttggta atgttctcac 540
43 ttctgctccg aacgccaaaa ccgttaatgg taaagctgaa agcagtgaca gtggagccga 600
44 gtctgaggaa gaagaggccc aagaagaagt gaaaggagca gaacaaagtg ataatgataa 660
45 gaaaatgatg aagaagtcag cagaccataa gaatttggaa gtcattgtca ctaatggcta 720
46 tgataaagat ggctttgttc aggatataca gaatgacatt catgccagtt cttccctgaa 780
47 tggcagaagc actgaagaag taaagcccat tgatgaaaac ttggggcaaa ctggaaaatc 840
48 tgctgtttgc attcaccaag atataaatga tgatcatgtt gaagatgtta caggaattca 900
49 gcatttgaca agcgattcag acagtgaagt ttactgtgat tctatggaac aatttggaca 960
50 agaagagtct ttagacagct ttacgtccaa caatggacca tttcagtatt acttgggtgg 1020
51 tcattccagt caacccatgg aaaattctgg atttcgtgaa gatattcaag tacctcctgg 1080
52 aaatggcaac attgggaata tgcaggtggt tgcagttgaa ggaaaaggtg aagtcaagca 1140
53 tggaggagaa gatggcagga ataacagcgg agcaccacac cgggagaagc gaggcggaga 1200
54 aactgacgaa ttctctaatg ttagaagagg aagaggacat aggatacaac acttgagcga 1260
55 aggaaccaag ggccggcagg tgggaagtgg aggtgatggg gagcgctggg gctccgacag 1320
56 agggtcccga ggcagcctca atgagcagat cgccctcgtg ctgatgagac tgcaggagga 1380
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57 catgcagaat gtccttcaga gactgcagaa actggaaacg ctgactgctt tgcaggcaaa 1440
58 atcatcaaca tcaacattgc agactgctcc tcagcccacc tcacagagac catcttggtg 1500
59 gcccttcgag atgtctcctg gtgtgctaac gtttgccatc atatggcctt ttattgcaca 1560
60 gtggttggtg tatttatact atcaaagaag gagaagaaaa ctgaactgag gaaaatggtg 1620
61 ttttcctcaa gaagactact ggaactggat gacctcagaa tgaactggat tgtggtgttc 1680
62 acaagaaaat cttagtttgt gatgattaca ttgctttttg ttgtccagta gtttagtttg 1740
63 tgtacat                                                        1747
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66 <210> SEQ ID NO: 2
67 <211> LENGTH: 523
68 <212> TYPE: PRT
69 <213> ORGANISM: Homo sapiens
71 <400> SEQUENCE: 2

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76              20                  25                  30
78 Glu Met Ala Asp Thr Arg Ser Val His Glu Thr Arg Phe Glu Ala Ala
79          35                  40                  45
81 Val Lys Val Ile Gln Ser Leu Pro Lys Asn Gly Ser Phe Gln Pro Thr
82      50                  55                  60
84 Asn Glu Met Met Leu Lys Phe Tyr Ser Phe Tyr Lys Gln Ala Thr Glu
85  65                  70                  75                  80
87 Gly Pro Cys Lys Leu Ser Arg Pro Gly Phe Trp Asp Pro Ile Gly Arg
88                  85                  90                  95
90 Tyr Lys Trp Asp Ala Trp Ser Ser Leu Gly Asp Met Thr Lys Glu Glu
91              100                 105                 110
93 Ala Met Ile Ala Tyr Val Glu Glu Met Lys Lys Ile Ile Glu Thr Met
94          115                 120                 125
96 Pro Met Thr Glu Lys Val Glu Glu Leu Leu Arg Val Ile Gly Pro Phe
97      130                 135                 140
99 Tyr Glu Ile Val Glu Asp Lys Lys Ser Gly Arg Ser Ser Asp Ile Thr
100 145                 150                 155                 160
102 Ser Asp Leu Gly Asn Val Leu Thr Ser Ala Pro Asn Ala Lys Thr Val
103                 165                 170                 175
105 Asn Gly Lys Ala Glu Ser Ser Asp Ser Gly Ala Glu Ser Glu Glu Glu
106                 180                 185                 190
108 Glu Ala Gln Glu Glu Val Lys Gly Ala Glu Gln Ser Asp Asn Asp Lys
109             195                 200                 205
111 Lys Met Met Lys Lys Ser Ala Asp His Lys Asn Leu Glu Val Ile Val
112     210                 215                 220
114 Thr Asn Gly Tyr Asp Lys Asp Gly Phe Val Gln Asp Ile Gln Asn Asp
115 225                 230                 235                 240
117 Ile His Ala Ser Ser Ser Leu Asn Gly Arg Ser Thr Glu Glu Val Lys
118                 245                 250                 255
120 Pro Ile Asp Glu Asn Leu Gly Gln Thr Gly Lys Ser Ala Val Cys Ile
121                 260                 265                 270
123 His Gln Asp Ile Asn Asp Asp His Val Glu Asp Val Thr Gly Ile Gln
124             275                 280                 285
126 His Leu Thr Ser Asp Ser Asp Ser Glu Val Tyr Cys Asp Ser Met Glu
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130 305                   310                   315                   320
132 Pro Phe Gln Tyr Tyr Leu Gly Gly His Ser Ser Gln Pro Met Glu Asn
133                   325                   330                   335
135 Ser Gly Phe Arg Glu Asp Ile Gln Val Pro Pro Gly Asn Gly Asn Ile
136                   340                   345                   350
138 Gly Asn Met Gln Val Val Ala Val Glu Gly Lys Gly Glu Val Lys His
139             355                   360                   365
141 Gly Gly Glu Asp Gly Arg Asn Asn Ser Gly Ala Pro His Arg Glu Lys
142       370                   375                   380
144 Arg Gly Gly Glu Thr Asp Glu Phe Ser Asn Val Arg Arg Gly Arg Gly
145 385                   390                   395                   400
147 His Arg Ile Gln His Leu Ser Glu Gly Thr Lys Gly Arg Gln Val Gly
148                   405                   410                   415
150 Ser Gly Gly Asp Gly Glu Arg Trp Gly Ser Asp Arg Gly Ser Arg Gly
151             420                   425                   430
153 Ser Leu Asn Glu Gln Ile Ala Leu Val Leu Met Arg Leu Gln Glu Asp
154             435                   440                   445
156 Met Gln Asn Val Leu Gln Arg Leu Gln Lys Leu Glu Thr Leu Thr Ala
157       450                   455                   460
159 Leu Gln Ala Lys Ser Ser Thr Ser Thr Leu Gln Thr Ala Pro Gln Pro
160 465                   470                   475                   480
162 Thr Ser Gln Arg Pro Ser Trp Trp Pro Phe Glu Met Ser Pro Gly Val
163                   485                   490                   495
165 Leu Thr Phe Ala Ile Ile Trp Pro Phe Ile Ala Gln Trp Leu Val Tyr
166             500                   505                   510
168 Leu Tyr Tyr Gln Arg Arg Arg Arg Lys Leu Asn
169             515                   520
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174 <212> TYPE: PRT
175 <213> ORGANISM: Homo sapiens
177 <220> FEATURE:
178 <221> NAME/KEY: VARIANT
179 <222> LOCATION: (3)
180 <223> OTHER INFORMATION: Wherein Xaa is any amino acid as defined in the
181       specification
183 <400> SEQUENCE: 3
W--> 184 Met Tyr Xaa Phe His Ala Gly Ser Trp Glu Ser Trp Cys Cys Cys Cys
185    1            5                   10                  15
187 Leu Ile Pro Ala Asp Arg Pro Trp Asp Arg Gly Gln His Trp Gln Leu
188             20                  25                  30
190 Glu Met Ala Asp Thr Arg Ser Val His Glu Thr Arg Phe Glu Ala Ala
191             35                  40                  45
193 Val Lys Val Ile Gln Ser Leu Pro Lys Asn Asp Ser Phe Gln Pro Thr
194       50                  55                  60
196 Asn Glu Met Met Leu Lys Phe Tyr Ser Phe Tyr Lys Gln Ala Thr Glu
197 65                  70                  75                  80
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199 Gly Pro Cys Lys Leu Ser Arg Pro Gly Phe Trp Asp Pro Ile Gly Arg
200             85                  90                  95
202 Tyr Lys Trp Asp Ala Trp Ser Ser Leu Gly Asp Met Thr Lys Glu Glu
203             100             105                 110
205 Ala Met Ile Ala Tyr Val Glu Glu Met Lys Lys Ile Ile Glu Thr Met
206             115             120                 125
208 Pro Met Thr Glu Lys Val Glu Glu Leu Leu Arg Val Ile Gly Pro Phe
209         130             135                 140
211 Tyr Glu Ile Val Glu Asp Lys Lys Ser Gly Arg Ser Ser Asp Ile Thr
212 145                 150                 155                 160
214 Ser Val Arg Leu Glu Lys Ile Ser Lys Cys Leu Glu Asp Leu Gly Asn
215             165                 170                 175
217 Val Leu Thr Ser Thr Pro Asn Ala Lys Thr Val Asn Gly Lys Ala Glu
218             180             185                 190
220 Ser Ser Asp Ser Gly Ala Glu Ser Glu Glu Glu Ala Gln Glu Glu
221         195             200                 205
223 Val Lys Gly Ala Glu Gln Ser Asp Asn Asp Lys Lys Met Met Lys Lys
224     210             215                 220
226 Ser Ala Asp His Lys Asn Leu Glu Val Ile Val Thr Asn Gly Tyr Asp
227 225             230             235                 240
229 Lys Asp Gly Phe Val Gln Asp Ile Gln Asn Asp Ile His Ala Ser Ser
230             245             250                 255
232 Ser Leu Asn Gly Arg Ser Thr Glu Glu Val Lys Pro Ile Asp Glu Asn
233             260             265                 270
235 Leu Gly Gln Thr Gly Lys Ser Ala Val Cys Ile His Gln Asp Ile Asn
236             275             280                 285
238 Asp Asp His Val Glu Asp Val Thr Gly Ile Gln His Leu Thr Ser Asp
239         290             295                 300
241 Ser Asp Ser Glu Val Tyr Cys Asp Ser Met Glu Gln Phe Gly Gln Glu
242 305             310             315                 320
244 Glu Ser Leu Asp Ser Phe Thr Ser Asn Asn Gly Pro Phe Gln Tyr Tyr
245             325             330                 335
247 Leu Gly Gly His Ser Ser Gln Pro Met Glu Asn Ser Gly Phe Arg Glu
248             340             345                 350
250 Asp Ile Gln Val Pro Pro Gly Asn Gly Asn Ile Gly Asn Met Gln Val
251             355             360                 365
253 Val Ala Val Glu Gly Lys Gly Glu Val Lys His Gly Gly Glu Asp Gly
254     370             375                 380
256 Arg Asn Asn Ser Gly Ala Pro His Arg Glu Lys Arg Gly Gly Glu Thr
257 385             390             395                 400
259 Asp Glu Phe Ser Asn Val Arg Arg Gly Arg Gly His Arg Met Gln His
260             405             410                 415
262 Leu Ser Glu Gly Thr Lys Gly Arg Gln Val Gly Ser Gly Gly Asp Gly
263             420             425                 430
265 Glu Arg Trp Gly Ser Asp Arg Gly Ser Arg Gly Ser Leu Asn Glu Gln
266     435             440                 445
268 Ile Ala Leu Val Leu Met Arg Leu Gln Glu Asp Met Gln Asn Val Leu
269     450             455                 460
271 Gln Arg Leu Gln Lys Leu Glu Thr Leu Thr Ala Leu Gln Ala Lys Ser
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272 465                   470                 475                 480
274 Ser Thr Ser Thr Leu Gln Thr Ala Pro Gln Pro Thr Ser Gln Arg Pro
275                   485                 490                 495
277 Ser Trp Trp Pro Phe Glu Met Ser Pro Gly Val Leu Thr Phe Ala Ile
278                   500                 505                 510
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281           515                 520                 525
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284       530
287 <210> SEQ ID NO: 4
288 <211> LENGTH: 536
289 <212> TYPE: PRT
290 <213> ORGANISM: Homo sapiens
292 <400> SEQUENCE: 4
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297               20                  25                  30
299 Gln Leu Glu Met Ala Asp Thr Arg Ser Val His Glu Thr Arg Phe Glu
300           35                  40                  45
302 Ala Ala Val Lys Val Ile Gln Ser Leu Pro Lys Asn Gly Ser Phe Gln
303       50                  55                  60
305 Pro Thr Asn Glu Met Met Leu Lys Phe Tyr Ser Phe Tyr Lys Gln Ala
306  65                  70                  75                  80
308 Thr Glu Gly Pro Cys Lys Leu Ser Arg Pro Gly Phe Trp Asp Pro Ile
309               85                  90                  95
311 Gly Arg Tyr Lys Trp Asp Ala Trp Ser Ser Leu Gly Asp Met Thr Lys
312               100                 105                 110
314 Glu Glu Ala Met Ile Ala Tyr Val Glu Glu Met Lys Lys Ile Ile Glu
315           115                 120                 125
317 Thr Met Pro Met Thr Glu Lys Val Glu Glu Leu Leu Arg Val Ile Gly
318       130                 135                 140
320 Pro Phe Tyr Glu Ile Val Glu Asp Lys Lys Ser Gly Arg Ser Ser Asp
321 145                 150                 155                 160
323 Ile Thr Ser Val Arg Leu Glu Lys Ile Ser Lys Cys Leu Glu Asp Leu
324               165                 170                 175
326 Gly Asn Val Leu Thr Ser Thr Pro Asn Ala Lys Thr Val Asn Gly Lys
327               180                 185                 190
329 Ala Glu Ser Ser Asp Ser Gly Ala Glu Ser Glu Glu Glu Ala Gln
330           195                 200                 205
332 Glu Glu Val Lys Gly Ala Glu Gln Ser Asp Asn Asp Lys Lys Met Met
333       210                 215                 220
335 Lys Lys Ser Ala Asp His Lys Asn Leu Glu Val Ile Val Thr Asn Gly
336 225                 230                 235                 240
338 Tyr Asp Lys Asp Gly Phe Val Gln Asp Ile Gln Asn Asp Ile His Ala
339               245                 250                 255
341 Ser Ser Ser Leu Asn Gly Arg Ser Thr Glu Glu Val Lys Pro Ile Asp
342               260                 265                 270
344 Glu Asn Leu Gly Gln Thr Gly Lys Ser Ala Val Cys Ile His Gln Asp
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 10/21/2002
PATENT APPLICATION: US/09/997,425   TIME: 16:04:03

Input Set : A:\Cura475c.app
Output Set: N:\CRF4\10212002\I997425.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos. 3